

097000 290260

Figure 1

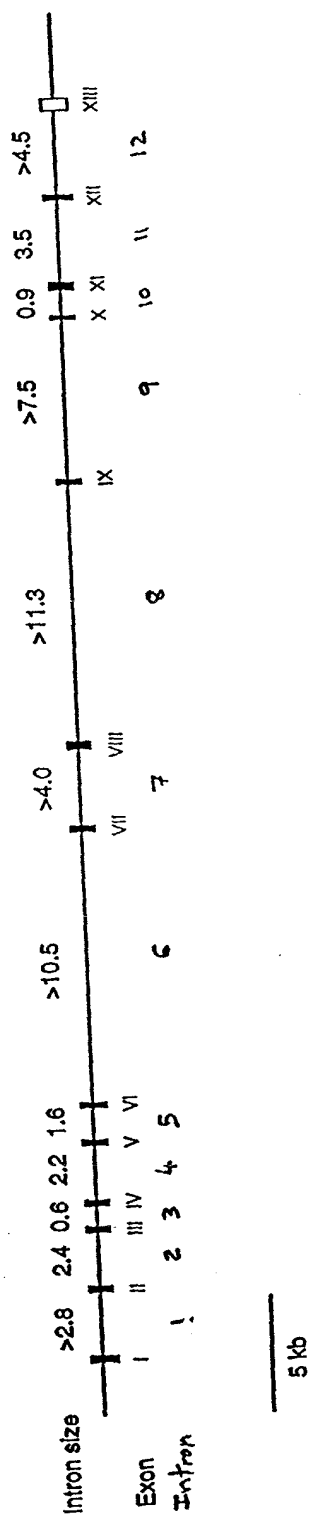


Figure 2A

promoter and exon 1

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CCCGATAGAGGAGGAGAGGGAGGAGGAGGGAAAAGGAAG
GGTGAGGGGCTCAGAGGGGAGAGCTGGGAGGAGGGGAGA
CATAGGTGGGGGAAGGGGTAGGAGAAAAGGGGAAGGGAGC
AAGAGGGTGAGGGGCACCAGGCCCCATAGACGTTTGGC
TCAGCGGCCACGAGGCTTCATCAGCTCCCGCCCCAAAAC
GGAAGCGAGGCCGTGGGGGCAGCGGCAGCATGGCGGGGC
TTGTCTTGGCGGCCATGGCCCCGCCCCCTGCCCGTCCGA
TCAGCGCCCCGCCCCGTCCCCGCCCCGACCCCGCCCCGG
GCCCGCTCAGGCCCCGCCCCGTGCCCGCCGAATCCTGAAG
CCCAAGGCTGCCCGGGGGCGGTCCCGCGGCGCCGGCGAT
GGGGCATAAAACCACTGGCCACCTGCCGGGCTGCTCC

TGCGTGCGCTGCCGTCCCGGATCCACCGTGCCTCTGCGG
CCTGCGTGCCCGGAGTCCCCGCCTGTGTCTCTCTGTCTG
CCGTCCCCGTCTCCTGCCAGGCGCGGAGCCCTGCCGAGCC
GCGGGTGGGCCCCAGGCGCGCAGACATGGCTGCTCCGC
CAAAGCGCGCTGGGCTGCCGGGGCGCTGGGCGTCCGCGG
GCTACTGTGCGCTGTGCTGGGCGCTGTCATGATCGTGAT
GGTGCCGTTCGCTCATCAAGCAGCAGGTCCTTAAG

A

GTGGGTGAGGGAGACCCAGGGGGTCCGCGCACGGACCC
GGGCTGTTGGGCGCTGGGCGCCGGGAGGACCCGCGCGTT
GCGGTGGGTGGGCGACCGCAGCGGAATCGGCGCCCGGGC
CTGGCGCCGCAGAACACGAGGGAGGCCAGGCGCTTCGGG
AGGGGCTGCTGCCCGCCTCCCCACCACCCTCACC

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Figure 2B

exon 2

AGCCTCATGTGCGAAGGGCTTTCCCACCACCTCCTATCC
CAAGCTCCCGCCGAGGAGCCCCCTCCCTGGCCGGGCTCG
GGCAGCTGTTCCGGAGCCTTGTGGTGGGGCGTGGGGCC
CTCATCACTCTCCTCACAAAGCGTACTTGTCCCTTCCC
CTGCAG

AACGTGCGCATCGACCCCAGTAGCCTGTCCTTCAACATG
TGGAAGGAGATCCCTATCCCCCTTCTATCTCTCCGTCTAC
TTCTTTGACGTCATGAACCCAGCGAGATCCTGAAGGGC
GAGAAGCCGCAGGTGCGGGAGCGCGGGCCCTACGTGTAC
AG

GTGAGGCTGTGTCCACGTGATGGTGGACGGGCCGGCTGA
CGCTGGGCATGGGACGGGTCTCANAGTGGACGGGATG
GGGAGGCTGCTGACTGACCCCCAAACATTGTTCCGGAA
GCACGCAACTCATAGTCGGGGTAAGTGCTACTCCCCAAA
AAGTTTGCGT

exon 3

CATGTCCTGCAGTGGGCAGGCAGCGGGAGGGACAGACTT
GGCGAAGGGGCCGAGCTCAGCTTTGGCTGTGGGGCCGGA
GGTGTGCACAGACGTCCAGGGCCCCTGGTTCCCAGGCAG
GCATTGCAGGCGAGTAGAAGGGAAACGTCCCATGCAG
CGGGGCGGGGCGTCTGACCCACTGGCTTCCCCCACAG

GGAGTTCAGGCACAAAAGCAACATCACCTTCAACAACAA
CGACACCGTGTCTCTTCTCGAGTACCGCACCTTCCAGTT
CCAGCCCTCCAAGTCCCACGGCTCGGAGAGCGACTACAT
CGTCATGCCCAACATCCTGGTCTTG

A

GTGAGGCTGCCCTGTGGCCACGCCGCCTCGCACCCCTGA
CCTCGTCCCCTGTCTCTCTCTCCCGCCTGCCCTTGTG
CAGAGAGCAGTCCCTGAGGTGGTTCGGAGCGTGGGGACTC
ACGCCTGGTGGGTGGCTTTTCGGCCCTGTGCTGTCTCCAC
CACCCCCA

Figure 2C

exon 4

GGTGGTTCTGGTGTCCCAGATGCCCCACGTGGCCACTCC
AGGGGCCCTCCTGCACCCCAGCATTTCCTTCATGGGCT
CTTTGCTGTGAGGCCAGCTGGGGCCAAGGGAGGATG
GGCCAGCCACGTCCAGCCTCTGACACTAGTGTCCCTTCG
CCTTGCAG

GGTGGCGCGGTGATGATGGAGAATAAGCCCATGACCCTG
AAGCTCATCATGACCTTGGCATTACACCACCTCGGCGAA
CGTGCCCTTCATGAACCGCACTGTGGGTGAGATCATGTGG
GGCTACAAGGACCCCTTGTGAATCTCATCAACAAGTACT
TTCCAGGCATGTTCCTTCAAGGACAAGTTCGGATTAT
TTGCTGAG

GTACGTGTGGCCTGGTGAGAAGCCAAAGATTCAGGCCTG
TGTCCCTGTCTTCCCCTCACACAGCCTGGACACTGGTC
ACCAGCTTGCTTTGTAGCTGGCTGGGGATCTAGTGGCTG
TGGGTGTAAAGTGAAGTGAAGAACCTGACTCAAACCGGCTT
GAGTGAAA

exon 5

CCTCTCGGTCCCCAGACACTGGGCATTTGGCAGTGAACC
AGATGCTGGGGGCCCTGTCCTTCTGGTGGAGGGGGAGGA
GGGCTCAGCCCAGAATGTTTACAGACCAGGCCGGCTCAA
TGGCAGGCCTAAGCCTTACGATGCTGTTCCCTGCTGTGT
CTGTAG

CTCAACAACCTCCGACTCTGGGCTCTTACGGTGTTACAG
GGGGTCCAGAACATCAGCAGGATCCACCTCGTGGACAAG
TGGAACGGGCTGAGCAAG

GTGAGGGGCGAGAGGCGAGGGCCCCCTGTGCCAGGGAGA
GGGGAGGGTGGGCCGCGCCATGGCTGCTCGGGAGTGGCA
GGGACCAGAGAGCTCCTTCTTCTTTGTGCTGAAGAG
GGTGCTGGGAGGATGAACACTCTTGAAGTTGGAGGAGGG
ATTTTA

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Figure 2D

exon 6

TCTCTGTGTGTCTACATAGCCTGCCCTCTTCCCACCGTG
CCAGTATTGGGAATTGAGTGGCCGTGCGTGCACCAGGGT
GAGTTAGGTGTGCAGCACCTGAGAGGGCTTATTAAGG
GGCCTTGGCCCTACTGAGGGGTCTAGTCTGGATGCTTCC
CCCCAG

GTTGACTTCTGGCATTCCGATCAGTGCAACATGATCAAT
GGAACCTTCTGGGCAAATGTGGCCGCCCTTCATGACTCCT
GAGTCCCTCGCTGGAGTCTACAGCCCGAGGCCTGCCG

GTAATCACTGGGACTCGGGGCCTCCTGGGTTCCTGGGT
AGCTCATGGCCAAATTCTGTGGTGTGGCTGTGCACCT
GGAAAGCATTTTGAATCATCGTGGATTTGAATCAGTAG
CCCTTGGCACCAGCTTGAATTCCTTTGGTACACCACC
AAAAGC

exon 7

GGAGGTGCGTGCAGCTCCGCGGGTGAGAGATGGGGGCGG
TTTGGACCCGGGAGGTGGTAGCGCCCGTGGGGAGAAGTG
GCTGGATCTGGGCAGCCTTTGGCAGGGCCTGGCTCTGGC
CGCCGGGTCTGGGTGTCCCCTCTCATCCTGTCTGTCC
CCTGCAG

ATCCATGAAGCTAATGTACAAGGAGTCAGGGGTGTTTGA
AGGCATCCCCACCTATCGCTTCGTGGCTCCCCAAAACCT
GTTTGCCAACGGGTCCATCTACCCACCCAACGAAGGCTT
CTGCCCCTGCCCTGGAGTCTGGAATTCAGAACGTCAGCAC
CTGCAGGTTCA

GTACGTGCCGTCCCCCTGTTCTGGGATNGCCGGAGGGTGT
TAGGTNTNGGGCACCTNANGGTTTATCTGCCCAATGCTG
TCTGCTTAATCTCTGGCCTCTGTACTCTTGATAACC
CATTAAGCCAAAAATATGATGCCTCTGGGACGATATCTG

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Figure 2E

exon 8

TGGGGCTTTTACAGAATGGAGGAAGGGATCCTCTCT
GTCGGGTATTATGGTCATCGCCACGGGGGTGCCGTGCAG
ACCACAGCTCTGTGCAGACTTCCGGAGTGGCAGGACGTG
CCAATATACTGTCGTTGTATGATGTCCCTCCCTGCCCT
TGTGTAG

GTGCCCCCTGTTTCTCTCCCATCCTCACTTCCTCAACG
CTGACCCGGTTCGGCAGAAAGCGGTGACTGGCCTGCACC
CTAACGAGGAGGCACACTCCTTGTTCCTGGACATCCACC
CG

GTGAGCCCCTGCCATCCTCTGTGGGGGGTGGGTGATTCC
TGGTTGGAGCACACCTGGCTGCCTCCTCTCTCCCAG
GCAGAGAGCTGCTGTGGGCTGGGGTGGTGGGAAGCCTGG
CTTCTAGAATCTCGAGCCACCAAAGTTCCTTACT

exon 9

CCCCAGCCTGTGGCTTGTTTTAGGTAAGATACAAGCAAG
CTCCACTGGGCAGTTAGCTGGGACGCCACCCTCTTGAC
TGGGACCAGGGAAAAGAAGGTGACTGTGTCCCTGGA
GCTTGGGGGTGGCCAGTCTCCTCACTGTGTTTGTGCCG
CAG

GTCACGGGAATCCCCATGAACTGCTCTGTGAAACTGCAG
CTGAGCCTCTACATGAAATCTGTCCGAGGCATTGG

GTGAGTGGGGACTGGGAAGTGGGGCTGCATTGCTCATTG
AGAGATTANGTGCTCAGTGCTCCAGTGTTCCCAGAC
TCCCCTGACATACCCAGGAAACAGGGCATGGGGAAGGG
AGAGGGTCCTATTGGGGGTGGAATCCAGTCCCTGCTGAT
CTTCTC

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Figure 2F

exon 10

ATGGCTCCTAAAGTGTTTCAGCTCATTGTTTATATTGG
TGGTGAGGGTTTAGTGTGTGCAAAATTATACTAAACC
TGTTTAGATGTTGTATTCAAGCAGAATTAGATCAAGTTT
GGGTGTAAGACTTTGTTCCAACACCTATGTCTTGCTTAT
TTCCAG

ACAAACTGGGAAGATTGAGCCTGTGGTCCTGCCGCTGCT
CTGGTTTGCAGAG

GTAAGGGTGCGTTGGGCACAGCGTCGGGGGCTTTTGTTA
ATAGCCAATGTGGGCATTTGAGGCAGGAGGCGGGGGG
AGCACCTTGTAAGAAAGGGAGAGGGCTGAGCCAGGGTAAC
CGGACTGTTACATGGACCAGCGTATCATACTTCACCC
TGTC

exon 11

CCTGGAGGGAGGAGGTCCCTGGCAGGCTCCAACACATGC
TTTAGCCGGGAAGCTTGAGGTGGGGAAAAGCTGAGGCGG
GCACAGAGGAAGGTGTTGGGTGGCATCTGCGCTGTAG
CCCGCAGCGTGGCGCCCCAGCTCATGTGTTTGTCAATTCT
GTCTCCTCAG

AGCGGGGCCATGGAGGGGGAGACTCTTCACACATTCTAC
ACTCAGCTGGTGTTGATGCCCAAGGTGATGCACTATGCC
CAGTACGTCCCTCCTGGCGCTGGGCTGCGTCCTGCTGCTG
GTCCCTGTCATCTGCCAAATCCGGAGCCAA

GTAGGTGCTGGCCAGAGGGCAGCCCGGGCTGACAGCCAT
TCGCTTGCCTGCTGGGGGAAAGGGGCCTCAGATCGGACC
CTCTGGCCAACCGCAGCCTGGAGCCCACCTCCAGCAG
CAGTCCTGCGTCTCTGCCGGAGTGGGAGCGGTCACTGCT
GGGGG

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Figure 2G

exon 12

CCCCACATCTCAGCCACCTGCAATCGTTGAGGGTTGTTG
GACTCTAAACTTATGTGCCTTTCCTGTTTCCTCTTTGCC
TTTTGCAAATTGAAGAACCGTGTA AAACCATTTTTAT
GTGGCTTCAACGTCAACTATAAATTAGCTTGGTTATCTT
CTAG

GAGAAATGCTATTTATTTGGAGTAGTAGTAAAAAGGGC
TCAAAGGATAAGGAGGCCATTCAGGCCTATTCTGAATCC
CTGATGACATCAGCTCCCAAGGGCTCTGTGCTGCAGGAA
GCAAAACTGTAG

GTGGGTACCAGGTAATGCCGTGCGCCTCCCCGCCCCCTC
CCATATCAAGTAGAATGCTGGCGGCTTAAACATTTGGG
GTCCTGCTCATTTCCTCAGCCTCAACTTCACCTGGAG
TGTCTACAGACTGAAGATGCATATTTGTGTATTTTGCTT
TTGGAGAAA

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Figure 3A

ACCGTGCTCTGGGGCTGCGTGCCCGGAGTCCCGGCTGTGTCTCTGTGCGCGTCCCGCTCTCTGCCAGGCGGG 79

GAGCCCTGCGAGCGCGGGTGGGCCCCAGGCGGCGAGAC ATG GGC TGC TCC GCC AAA GCG GCG TGG GCT 148

A G A L G V A G L L C A V L G A V M I V 30
GCC GGG GCG CTG GGC GTC GCG GGG CTA CTG TGC GCT GTG CTG GGC GCT GTC ATG ATC GTG 208

exon 1 → exon 2

H V P S L I K Q Q V L K N V R I D P S S 50
ATG GTG CCG TCG CTC ATC AAG CAG CAG GTC CTT AAG AAC GTG GCG ATC GAC CCC AGT AGC 268

L S F N M W K E I P I P F Y L S V Y F F 70
CTG TCC TTC AAC ATG TGG AAG GAG ATC CCT ATC CCC TTC TAT CTC TCC GTC TAC TTC TTT 328

D V M N P S E I L K G E K P Q V R E R G 90
GAC GTC ATG AAC CCC AGC GAG ATC CTG AAG GGC GAG AAG CCG CAG GTG GCG GAG GCG GGG 388

exon 3

P Y V Y R E F R H K S N I T F N N N D T 110
CCC TAC GTG TAC AGG GAG TTC AGG CAC AAA AGC AAC ATC ACC TTC AAC AAC AAC GAC ACC 448

V S F L E Y R T F Q F Q P S K S H G S E 130
GTG TCC TTC CTC GAG TAC GCG ACC TTC CAG TTC CAG CCC TCC AAG TCC CAC GGC TCG GAG 508

exon 4

S D Y I V M P N I L V L G A A V H M E N 150
AGC GAC TAC ATC GTC ATG CCC AAC ATC CTG GTC TTG GGT GCG GCG GTG ATG ATG GAG AAT 568

K P M T L K L I H T L A F T T L G E R A 170
AAG CCC ATG ACC CTG AAG CTC ATC ATG ACC TTG GCA TTC ACC ACC CTC GGC GAA CGT GCC 628

F M N R T V G E I M W G Y K D P L V N L 190
TTC ATG AAC CGC ACT GTG GGT GAG ATC ATG TGG GGC TAC AAG GAC CCC CTT GTG AAT CTC 688

exon 5

I N K Y F P G M F P F K D K F G L F A E 210
ATC AAC AAG TAC TTT CCA GGC ATG TTC CCC TTC AAG GAC AAG TTC GGA TTA TTT GCT GAG 748

L N N S D S G L F T V F T G V Q N I S R 230
CTC AAC AAC TCC GAC TCT GGG CTC TTC ACG GTG TTC ACG GGG GTC CAG AAC ATC AGC AGG 808

exon 6

I H L V D K W N G L S K V D F W H S D Q 250
ATC CAC CTC GTG GAC AAG TGG AAC GGG CTG AGC AAG GTT GAC TTC TGG CAT TCC GAT CAG 868

C N M I N G T S G Q M W P P F M T P E S 270
TGC AAC ATG ATC AAT GGA ACT TCT GGG CAA ATG TGG CCG CCC TTC ATG ACT CCT GAG TCC 928

exon 7

S L E F Y S P E A C R S M K L M Y K E S 290
TCG CTG GAG TTC TAC AGC CCG GAG GCC TGC CGA TCC ATG AAG CTA ATG TAC AAG GAG TCA 988

G V F E G I P T Y R F V A P K T L F A N 310
GGG GTG TTT GAA GGC ATC CCC ACC TAT GCG TTC GTG GCT CCC AAA ACC CTG TTT GCC AAC 1048

G S I Y P P N E G F C P C L E S G I Q N 330
GGG TCC ATC TAC CCA CCC AAC GAA GGC TTC TGC CCG TGC CTG GAG TCT GGA ATT CAG AAC 1108

exon 8

V S T C R F S A P L F L S H P H F L N A 350
GTC AGC ACC TGC AGG TTC AGT GCC CCC TTG TTT CTC TCC CAT CCT CAC TTC CTC AAC GC 1168

D P V L A E A V T G L H P N Q E A H S L 370
GAC CCG GTT CTG GCA GAA GCG GTG ACT GCC CTG CAC CCT AAC CAG GAG GCA CAC TCC TTG 1228

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Figure 3B

F L D I H P V T G I P M N C S V K L Q L 390
 TTC CTG GAC ATC CAC CCG GTC ACG GGA ATC CCC ATG AAC TGC TCT GTG AAA CTG CAG CTG 1288
 S L Y M K S V A G I G Q T G K I E P V V 410
 AGC CTC TAC ATG AAA TCT GTC GCA GGC ATT GGA CAA ACT GGG AAG ATT GAG CCT GTG GTC 1348
 L P L L W F A E S G A M E G E T L H T F 430
 CTG CCG CTG CTC TGG TTT GCA GAG AGC GGG GCC ATG GAG GGG GAG ACT CTT CAC ACA TTC 1408
 Y T Q L V L M P K V M H Y A Q Y V L L A 450
 TAC ACT CAG CTG GTG TTG ATG CCC AAG GTG ATG CAC TAT GCC CAG TAC GTC CTC CTG GCG 1468
 L G C V L L L V P V I C Q I R S Q E K C 470
 CTG GGC TGC GTC CTG CTG CTG GTC CCT GTC ATC TGC CAA ATC CGG AGC CAA GAG AAA TGC 1528
 Y L F W S S S K K G S K D K E A I Q A Y 490
 TAT TTA TTT TGG AGT AGT AGT AAA AAG GGC TCA AAG GAT AAG GAG GCC ATT CAG GCC TAT 1588
 S E S L M T S A P K G S V L Q E A K L * 510
 TCT GAA TCC CTG ATG ACA TCA GCT CCC AAG GGC TCT GTG CTG CAG GAA GCA AAA CTG TAG 1643
 GGTCCTGAGGACACCGTGAGCCAGCCAGGCGCTGGCGCTGGGCTGACCGGCCCCCAGCCCTACACCCCGCTTCTCC 1727
 CGGACTCTCCAGCAGACAGCCCCCAGCCCCACAGCCTGAGCCTCCAGCTGCCATGTGCCTGTTGCCACACCTGCACA 1806
 CACGCCCTGGCACACATACACATGCGTGCAGGCTTGTGCAGACACTCAGGATGGAGCTGCTGCTGAAGGGACTTGT 1955
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 TCCTGCGTCCCTTCTCTCGGGTGAGCCTGGCCTGTCCCGTTCAGCCGTTGGGCCAGGCTTCTTCCCTCCAAGGTGAA 2043
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 GGGGACTCAGTGCCAGGCCCTGGCCACGAGCTTTGGCCTTGGTCTACCTGCCAGGCCAGGCAAAGCGCCTTTACACAG 2231
 GCGTCGGAACAATGGAGTGAGCACAAGATGCCCTGTGCAGCTGCCCGAGGGTCTCGGCCACCCCGGCCGACTTTG 2230
 ATCCCCCGAAGTCTTACAGGCACTGCATCGGGTGTCTGGCGCCCTTTTCTCCAGCCTAAACTGACATCATCCTAT 2359
 GGACTGAGCCGGCCACTTCTTGGCCGAAGTGGCCGAGGCTGTGCCCGGAGCTGCCCCACCCCTCACAGGGTCCCT 2438
 CAGATTATAGGTGCCAGGCTGAGGTGAAGAGGCGCTGGGGCGCTGCGCTTCCGGGCGCTCCTGGACCTGGGGCAAACC 2517
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Figure 4

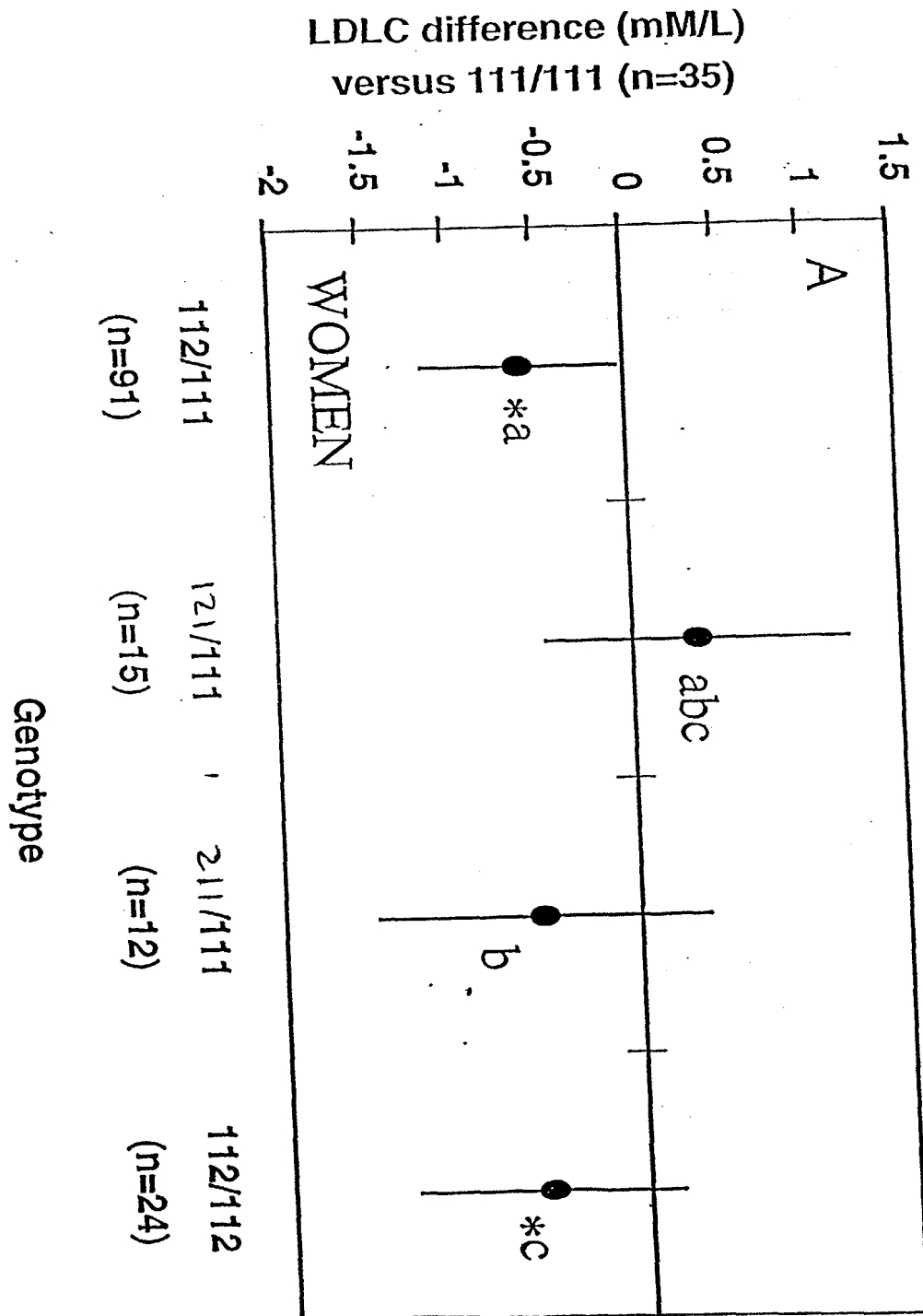
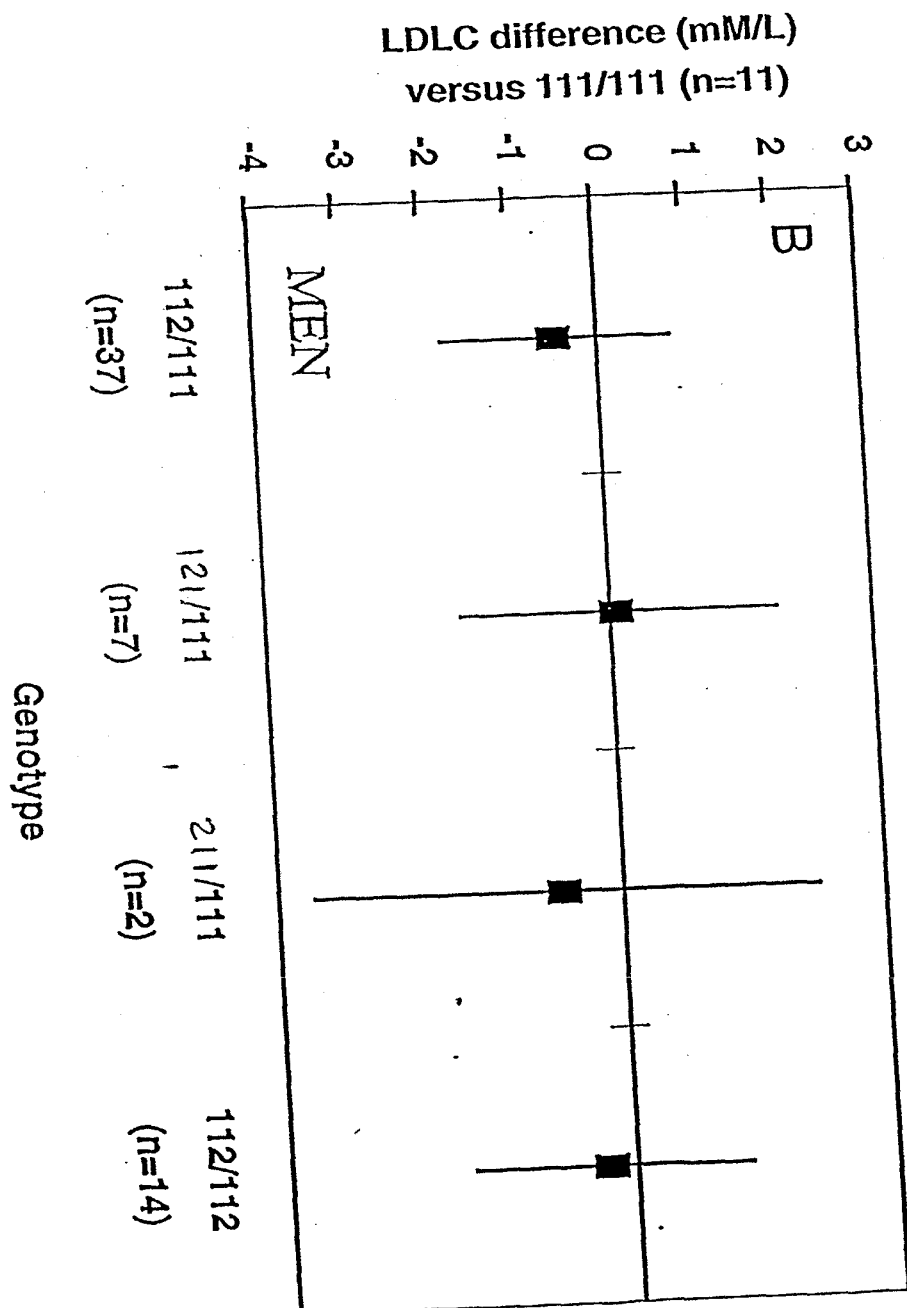
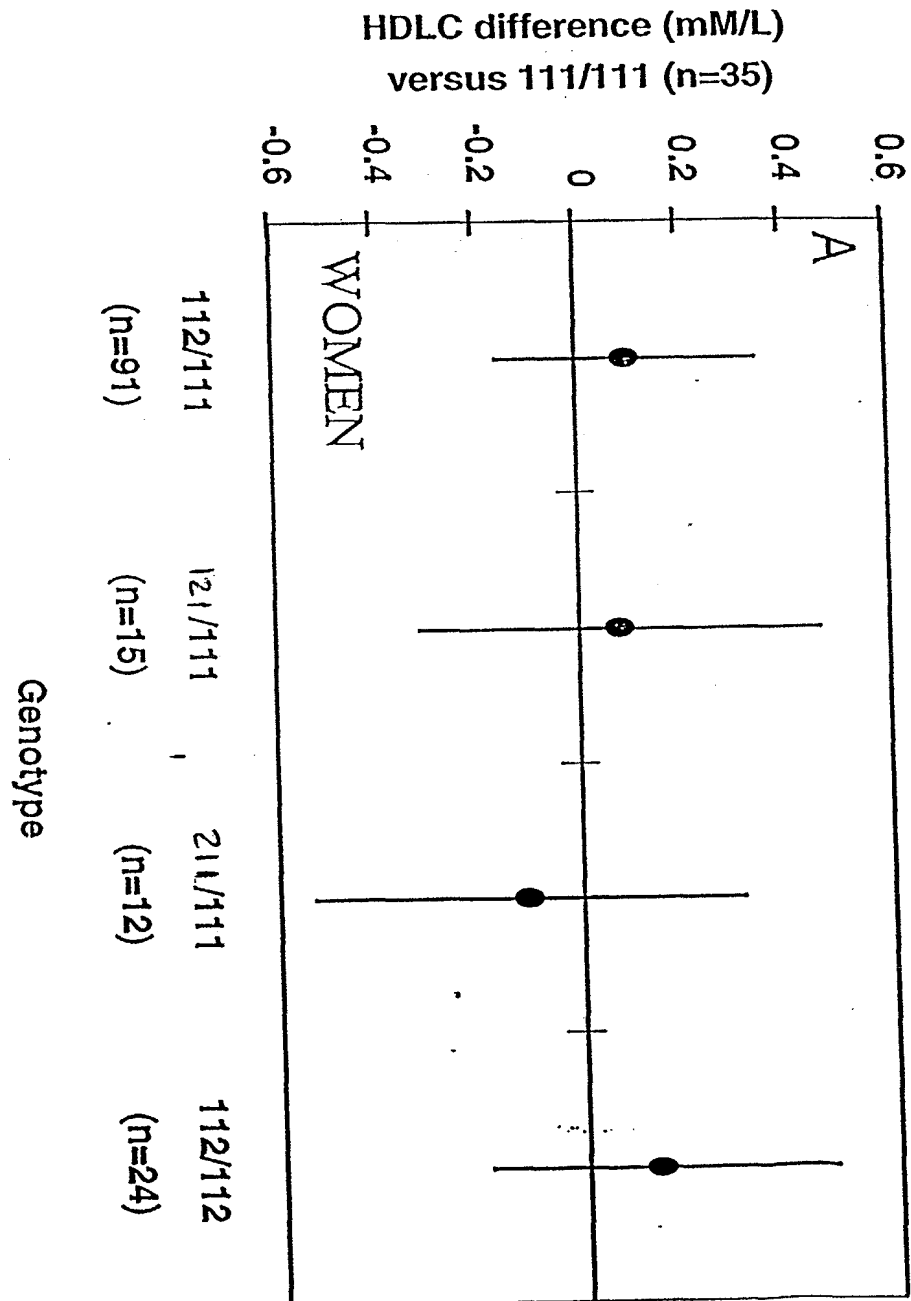


Figure 5



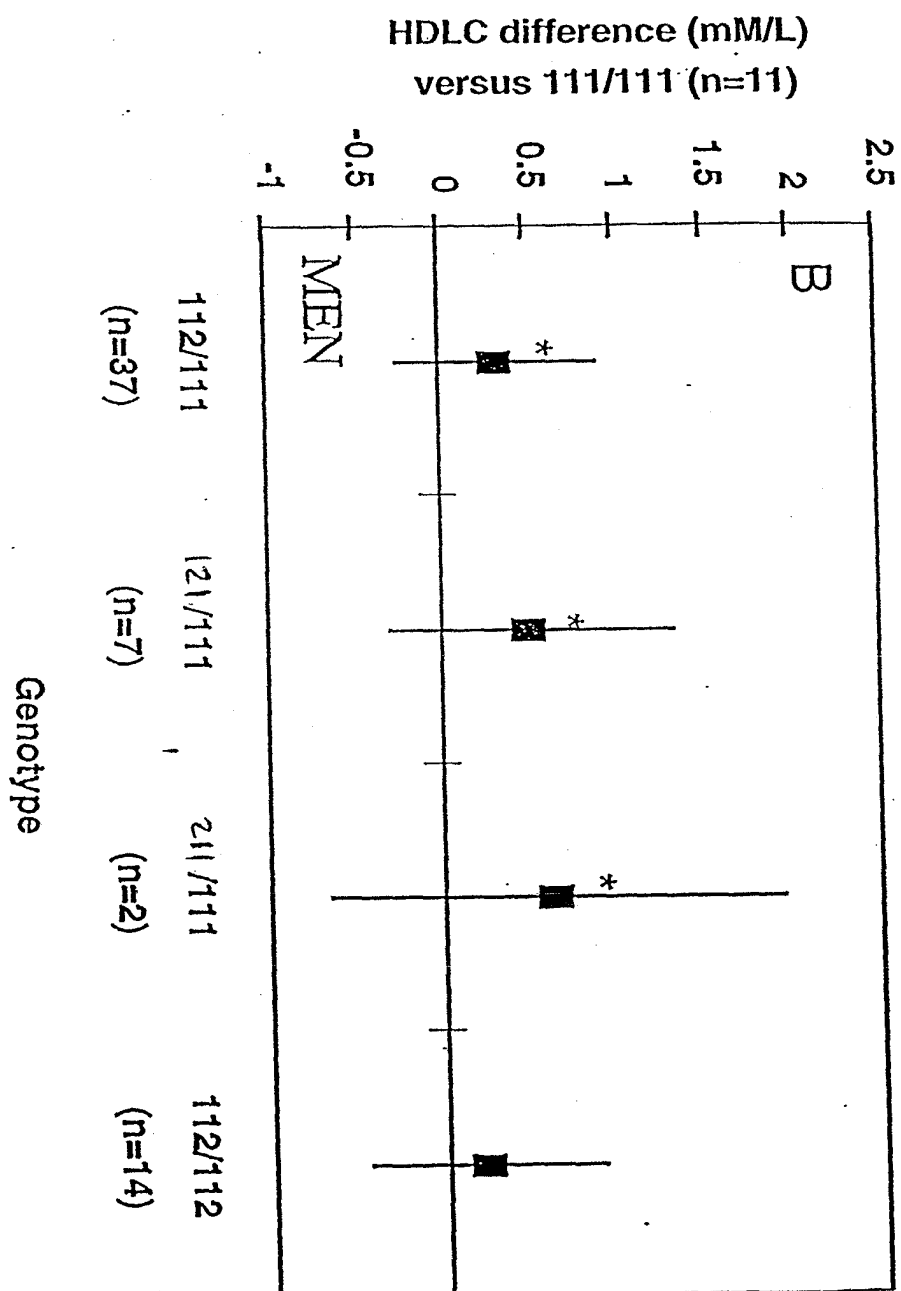
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Figure 6



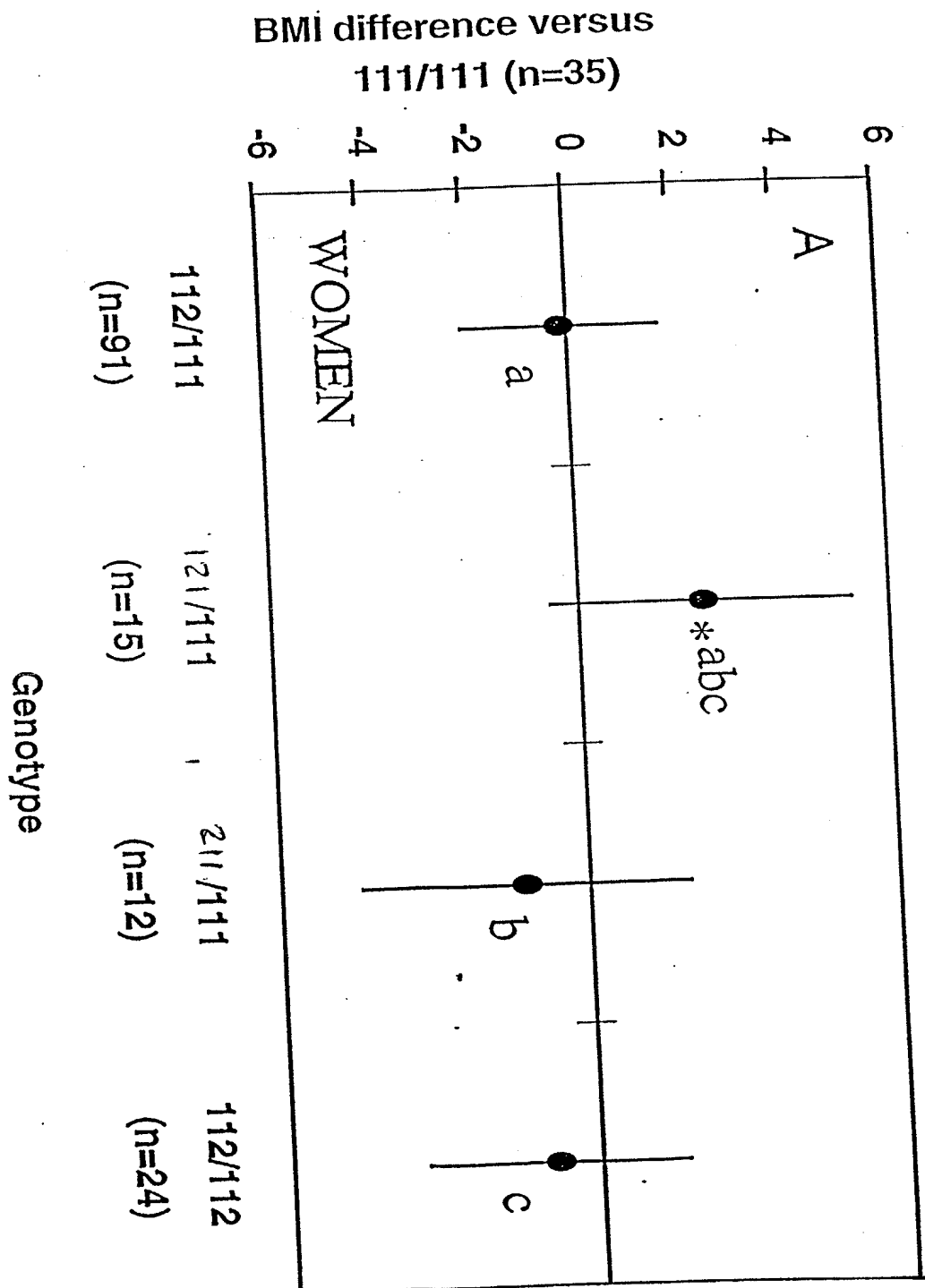
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Figure 7



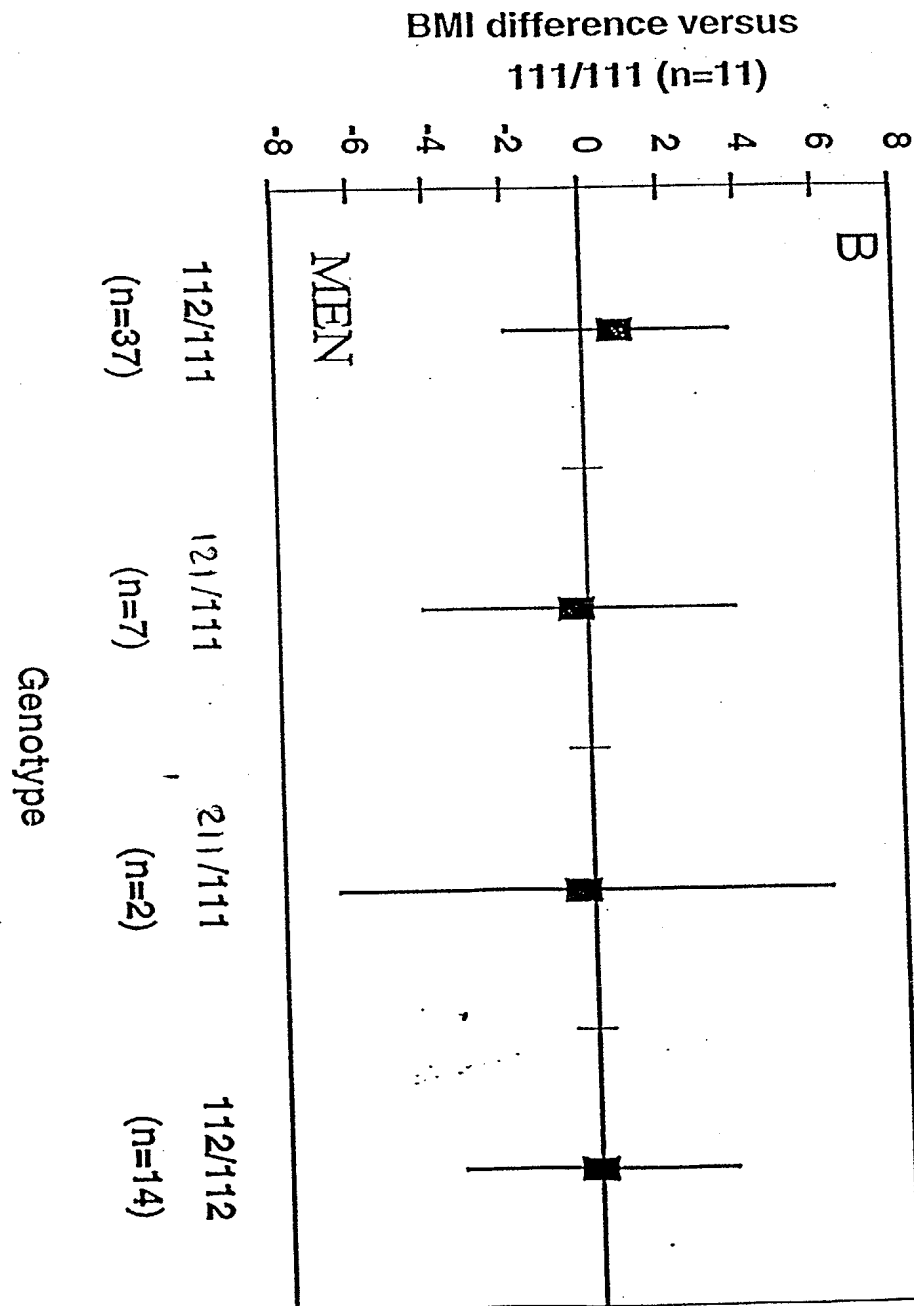
09770452 0000001

Figure 8



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Figure 9



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